variable. **CONCLUSIONS:** Logistic regression using a generalized multinomial logit link appears to provide a good propensity score from which pseudo-randomization into three groups can be performed in a retrospective sample.

PRM45

NETWORK META-ANALYSIS OF STUDIES WITH OUTCOMES AT MULTIPLE TIME POINTS USING FRACTIONAL POLYNOMIALS

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OBJECTIVES: Network meta-analysis of randomized controlled trials (RCTs) are often based on one effect measure per study. However, many studies have data available at multiple time points. Furthermore, not all studies might have measured the outcomes at the same time points. As an alternative to network meta-analysis based on the results at one time point, a network meta-analysis method is presented that allows for the simultaneous analysis of outcomes at multiple time points. **METHODS:** The development of outcomes over time of interventions compared in a RCT are modeled with fractional polynomials, and the difference between the parameters of these polynomials within a trial are synthesized across studies with a Bayesian network meta-analysis. **RESULTS:** The proposed models are illustrated with an analysis of RCTs evaluating interventions for osteoarthritis of the knee. Fixed and random effects first and second order fractional polynomials were evaluated. **CONCLUSIONS:** Network meta-analysis with models where the treatment effect is represented with several parameters using fractional polynomials can be used to simultaneously analyze results at multiple follow-up times that are not consistent across studies.

PRM46

CONTROLLING FOR MULTIPLICITY IN PURSUIT OF A PRO-BASED LABEL WHEN MULTIPLE PROS ARE ASSESSED

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OBJECTIVES: The FDA's final Guidance for industry on patient reported outcome (PRO) use in support of labeling claims was issued in December, 2009. In their Guidance, the FDA noted that a study's endpoint model must consider the hierarchy of multiple endpoints, including how PROs used for a label claim fit into this hierarchy. Whereas most studies implement a basic sequential gatekeeping process to articulate their hierarchy, this may place some potential labels at risk. Researchers should be knowledge of the various ways familywise error is influenced and how best to control for it with an informed multiplicity plan as part of their endpoint model. **METHODS:** Outcomes from previously published literature were examined for the influence of various familywise error issues and related multiplicity controls, including analytic issues, gatekeeping, and precision alpha control (vs. Bonferroni or Hochberg). **RESULTS:** In a study with one clinical and three PRO outcomes, A Bonferroni correction resulted in just one significant result. A gatekeep between primary and secondary outcomes resulted in two significant findings. Finally, when using either an adjustment for known-levels of correlation to adjust alpha (Tukey's test of statistical certainty) or using a repeated measures ANOVA vs. change-score analysis, three of the outcomes were classified as significant. **CONCLUSIONS:** Researchers should understand the implications of their multiplicity control in order to make informed decisions about their analyses, organization of their endpoint model, and ultimately make the best plans to ensure their desired PRO-based label claims have the most accurate demonstration of their statistical probability.

PRM47

BAYESIAN REGRESSION MODELS FOR ESTIMATION OF ILLNESS-ATTRIBUTABLE COST FROM AGGREGATE DATA

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OBJECTIVES: In Health Economics, the estimation of disease specific attributable cost is of major importance. For this estimation, cost data of cases (patients with the disease) and comparable controls (patients without the disease) are often utilized. When individual level data are available, regression and GLM models, addressing issues such as skeweness and heteroscedasticity, can be applied. When only aggregate level data (e.g. sample means and standard deviations per strata) are available, these models may not be appropriate. **METHODS:** Here, motivated by real pressure ulcer cost data, we propose and study a Bayesian Gamma regression mixed model that utilizes as stochastic nodes both sample means and inverse coefficients of variation. We investigate its performance and goodness of fit (using deviance) using various simulated data and compare it with two linear models, assuming known and unknown cost variances per stratum. We also use the method for estimating pressure ulcer attributable costs. **RESULTS:** In most cases, the linear models give more accurate estimates of the attributable cost, with significantly shorter computational time. The random effects adapt to the multiplicative nature of the data, posterior means between intercept and slope are positively correlated. **CONCLUSIONS:** When only aggregate data are available, the simplest linear model seems to estimate the attributable costs sufficiently well. The proposed Gamma model, despite being more theoretically justifiable, is of questionable benefit. Further investigation is needed for refining the Gamma model and selecting appropriate measures of model assessment and comparison.

PRM48

DIAGNOSTIC TOOLS FOR THE ASSESSMENT OF THE UNDERLYING MODEL ASSUMPTIONS IN THE STUDY OF HEALTH CARE COSTS

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OBJECTIVES: It is a common practice to use a log link and assume a gamma distribution when performing regressions of health care costs as an outcome on a set of potential predictors. In many circumstances, this approach is reasonable and performs well; however, do circumstances exist where these assumed model characteristics are untenable? If so, do simple diagnostic procedures exist that can assess the appropriateness of model assumptions for regression models involving cost as an outcome? **METHODS:** Application of residual analyses available in common statistical software packages (e.g., SAS) afford practitioners the ability to graphically and analytically evaluate whether the choice of a link is appropriate in a given cost model regression scenario. These same tools can also assist with an assessment of overall model fit. **RESULTS:** The author will juxtapose contrasting cases of where the choice of a generalized linear model with a log link and an assumed gamma distribution are defensible and where these assumptions are not met and may lead to errors in subsequent inference. **CONCLUSIONS:** With the use of these readily available diagnostic procedures found in common software packages it is possible to easily evaluate whether underlying model assumptions are tenable and if the choice of a simpler, more common approach may actually demonstrate higher fidelity to its underlying model assumptions than the commonly used generalized linear model with a gamma distribution and a log link.

PRM49

HOW TO PRESENT THE PROBABILITY OF BEING THE BEST TREATMENT IN THE CONTEXT OF A BAYESIAN NETWORK META-ANALYSIS OF PARAMETRIC SURVIVAL CURVES?

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OBJECTIVES: Increasingly, network meta-analysis (NMA) of published survival data are based on parametric survival curves as opposed to reported hazard ratios to avoid relying on the proportional hazards assumption, which may not be valid. One advantage of a Bayesian approach to NMA is that the probability of being the best treatment out of all those compared can be calculated. This directly supports decision-making. However, in the context of survival analysis multiple options are available. **METHODS:** Based on a case study in oncology, the probability that each treatment is best in terms of overall survival was calculated and presented based on the following underlying **RESULTS:** 1) the hazard over time, 2) the cumulative hazard over time, 3) the survival proportions over time, 4) the expected survival over time, 5) the expected survival at maximum follow-up, 6) expected survival when all patients have died, and 7) median survival. **RESULTS:** Since the NMA of survival curves results in changing hazard and survival estimates over time for the compared interventions, calculations of the probability that a certain treatment is best varies with the different alternatives. With methods 1-4 the probability that a certain treatment is best will vary as a function of follow-up, which provides relevant information. With methods 5-7 only one probability of being the best is obtained for each treatment, which is easier to understand. Method 1 does not directly relate to the survival proportion, which makes it not very intuitive. Method 7 discards a lot of information. **CONCLUSIONS:** Different approaches to present the probability of being the most efficacious treatment for findings obtained with a NMA of survival curves have pros and cons. The probability that a certain treatment is best as a function of survival proportions over time, as well as expected survival over time seem the most useful and intuitive.

PRM50

META-REGRESSION MODELS TO ADDRESS HETEROGENEITY AND INCONSISTENCY IN NETWORK META-ANALYSIS OF SURVIVAL OUTCOMES

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OBJECTIVES: As an alternative to network meta-analysis (NMA) of survival data based on the single constant hazard ratio (HR), NMA with a multi-dimensional treatment effect were introduced recently. With these models the HR is modeled as a function of time, and violations of the transitivity assumption are less likely. Bias is still present, however, if there are systematic differences in effect modifiers across comparisons. The objective of this paper is to extend multidimensional NMA models for survival data with treatment-by-covariate interactions to adjust for confounding bias. **METHODS:** By means of an example network of randomized controlled trials evaluating different interventions for melanoma, three different approaches for the analysis of overall survival (OS) are compared. 1) NMA assuming a constant HR between treatment and control group for each study; 2) a two-dimensional NMA model assuming survival outcomes are described by a Weibull function; and 3) an extension of method 2 with treatment-by-covariate interactions to adjust for systematic differences across studies. **RESULTS:** The models with the two-dimensional treatment effect (approach 2 and 3) fit more closely to the data than the model with the constant HR (approach 1). Adding treatment-by-covariate interactions for the scale parameter of the two-dimensional NMA models reduced inconsistency. **CONCLUSIONS:** Adding treatment-by-covariate interactions to multi-dimensional NMA models for published survival curves is worthwhile to explain systematic differences across studies and reduce inconsistencies. An additional advantage is that heterogeneity in survival data can be addressed.